

CLAIMS

We claim:

1. A method for measuring the amount of a target nucleic acid sequence in a biological sample, comprising the steps of:
 - a) preparing a sample by adding a known amount of a standard nucleic acid having a nucleotide sequence at least one base different than the target nucleic acid sequence to a biological specimen containing the target nucleic acid, thereby creating a site of differentiation between the target and the standard nucleic acid;
 - b) amplifying the sample of step a);
 - c) enhancing the difference between the standard and the target nucleic acid sequence at the site of differentiation; and
 - d) quantifying the enhanced products of step c) by measuring the ratio of the amplified target nucleic acid to the amplified standard nucleic acid to measure the amount of target nucleic acid sequence present in the biological sample.
2. The method of claim 1, wherein the target nucleic acid is from an infectious agent.
3. The method of claim 1, wherein the target nucleic acid is an mRNA transcript.
4. The method of claim 1, wherein the quantifying is performed using MALDI-TOF mass spectrometry.
5. The method of claim 1, wherein step c) is performed using primer extension at the site of differentiation.
6. The method of claim 1, wherein step c) is performed using allele specific enzyme cleavage at the site of differentiation.
7. The method of claim 1, wherein step c) is performed using allele-specific hybridization at the site of differentiation.

6. The method of claim 1, 5, 6, and 7, wherein the quantifying is performed using MALDI-TOF mass spectrometry.
7. A kit comprising at least one standard nucleic acid designed to differ from at least one corresponding target nucleic acid contained in a tube, and instructions on how to use the standard in quantifying the amount of the corresponding target nucleic acid in a nucleic acid sample according to method of claim 1.